



0570  
1219

## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/927,811B  
Source: OIP  
Date Processed by STIC: 2/12/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202



Does Not Comply  
Corrected Diskette Needed

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/927,811B

DATE: 02/12/2003

TIME: 12:29:54

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\02122003\I927811B.raw

Please re-submit in  
the English  
language.

3 <110> APPLICANT: RheinBiotech Gesellschaft fur neue biotechnologische Prozesse  
4 und Produkte mbH  
6 Romano, Ivano  
8 Gellissen, Gerd  
10 DeVergilio, Claudio  
12 <120> TITLE OF INVENTION: Heat-Inducible Promoter  
14 <130> FILE REFERENCE: PCT1106-01966  
16 <140> CURRENT APPLICATION NUMBER: 09/927,811B  
C--> 18 <141> CURRENT FILING DATE: 2003-02-07  
20 <150> PRIOR APPLICATION NUMBER: PCT/EP00/01144  
22 <151> PRIOR FILING DATE: 2000-02-11  
E--> 24 <160> NUMBER OF SEQ ID NOS: (27) - found 28  
26 <170> SOFTWARE: PatentIn version 3.1

## ERRORED SEQUENCES

601 <210> SEQ ID NO: 28  
602 <211> LENGTH: 15  
603 <212> TYPE: DNA  
604 <213> ORGANISM: Saccharomyces cerevisiae  
W--> 605 <220> FEATURE:  
606 <223> OTHER INFORMATION: Heat shock element  
608 <400> SEQUENCE: 28  
609 ggaacagaaac aatcg  
W--> 611 (continued). (continued). (continued). (continued). (continued). (continued). (continued).  
(con  
W--> 612 tinued). (continued). (continued). (continued). (continued). (continued). (continued).  
(contin  
W--> 613 ed). (continued). (continued). (continued). (continued). (continued). (continued).  
(continued).  
W--> 614 continued). (continued). (continued). (continued). (continued). (continued). (continued).  
(cont  
W--> 615 inued). (continued). (continued). (continued). (continued). (continued). (continued).  
(continue  
W--> 616 d). (continued). (continued). (continued). (continued). (continued). (continued). (continued).  
(continued). (c  
W--> 617 ontinued). (continued). (continued). (continued). (continued). (continued). (continued).  
(conti  
W--> 618 nued). (continued). (continued). (continued). (continued). (continued). (continued).  
(continued  
W--> 619 ). (continued). (continued). (continued). (continued). (continued). (continued).  
(continued). (co  
W--> 620 ntinued). (continued). (continued). (continued). (continued). (continued). (continued).

delete

15

·(contin

W--> 621 ued) . (continued) . (continued) . (continued) . (continued) . (continued) . (continued) .  
(continued)

W--> 622 . (continued) . (continued) . (continued) . (continued) .

W--> 623 (8)

E--> 625 (1) -delete

} delete

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/927,811B

DATE: 02/12/2003  
TIME: 12:29:56

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF4\02122003\I927811B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:28; Line(s) 611,612,613,614,615,616,617,618,619,620,621

## VERIFICATION SUMMARY

DATE: 02/12/2003

PATENT APPLICATION: US/09/927,811B

TIME: 12:29:56

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\02122003\I927811B.raw

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:71 M:283 W: Missing Blank Line separator, <220> field identifier  
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
L:86 M:283 W: Missing Blank Line separator, <220> field identifier  
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:109 M:283 W: Missing Blank Line separator, <220> field identifier  
L:385 M:283 W: Missing Blank Line separator, <220> field identifier  
L:389 M:283 W: Missing Blank Line separator, <220> field identifier  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:402 M:283 W: Missing Blank Line separator, <220> field identifier  
L:404 M:283 W: Missing Blank Line separator, <220> field identifier  
L:416 M:283 W: Missing Blank Line separator, <220> field identifier  
L:430 M:283 W: Missing Blank Line separator, <400> field identifier  
L:440 M:283 W: Missing Blank Line separator, <400> field identifier  
L:447 M:283 W: Missing Blank Line separator, <220> field identifier  
L:484 M:283 W: Missing Blank Line separator, <400> field identifier  
L:494 M:283 W: Missing Blank Line separator, <400> field identifier  
L:552 M:283 W: Missing Blank Line separator, <400> field identifier  
L:563 M:283 W: Missing Blank Line separator, <400> field identifier  
L:585 M:283 W: Missing Blank Line separator, <400> field identifier  
L:605 M:283 W: Missing Blank Line separator, <220> field identifier  
L:611 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:612 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:612 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:613 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:613 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:614 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:615 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:615 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:616 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:616 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:617 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:617 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:618 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:618 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:619 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:619 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:620 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:620 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:621 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:621 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:622 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:622 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:623 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:625 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:24 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (27) Counted (28)